

Spacer	22%
Sixth EGF repeat	40%
"99aa spacer"	38%
Seventh EGF repeat	11% /NA
Eighth EGF repeat	44%
Ninth EGF repeat	29% /NA
Cysteine knot motif	34%

NA: not applicable due to absence of homologous repeat.

Figures for individual LLRs are shown in brackets.--

See 93  
Immediately prior to the claims, please insert the enclosed 23 page section entitled "SEQUENCE LISTING".

Please delete all pages after page 17.

#### IN THE CLAIMS

Please cancel all pending claims (1-7) and add new claims 8-27 as follows:

8. (New) A mixture comprising an isolated Slit polypeptide and a Robo polypeptide, said Slit polypeptide comprising at least one sequence selected from the group consisting of SEQ ID NOS:2-14, or a subsequence thereof having at least 16 consecutive amino acid residues thereof.

9. (New) A mixture according to claim 8, the <sup>first</sup> Slit polypeptide comprising at least one sequence selected from the group consisting of SEQ ID NOS:2-14, or a subsequence thereof having at least 64 consecutive amino acid residues thereof.

10. (New) A mixture according to claim 8, the <sup>first</sup> Slit polypeptide comprising at least one sequence selected from the group consisting of SEQ ID NOS:2-14.

11. (New) A mixture according to claim 8, the <sup>first</sup> Slit polypeptide comprising SEQ ID NO:2, or a subsequence thereof having at least 16 consecutive amino acid residues thereof.

12. (New) A mixture according to claim 8, the <sup>first</sup> Slit polypeptide comprising SEQ ID NO:2, or a subsequence thereof having at least 64 consecutive amino acid residues thereof.

13. (New) A mixture according to claim 8, the <sup>1st</sup> polypeptide comprising at least one sequence selected from the group consisting of SEQ ID NOS:3-6, or a subsequence thereof having at least 16 consecutive amino acid residues thereof.

14. (New) A mixture according to claim 8, the <sup>1st</sup> polypeptide comprising at least one sequence selected from the group consisting of SEQ ID NOS:3-6, or a subsequence thereof having at least 64 consecutive amino acid residues thereof.

15. (New) A mixture according to claim 8, the <sup>1st</sup> polypeptide comprising SEQ ID NO:7, or a subsequence thereof having at least 16 consecutive amino acid residues thereof.

16. (New) A mixture according to claim 8, the <sup>1st</sup> polypeptide comprising SEQ ID NO:7, or a subsequence thereof having at least 64 consecutive amino acid residues thereof.

17. (New) A mixture according to claim 8, the <sup>1st</sup> polypeptide comprising at least one sequence selected from the group consisting of SEQ ID NOS:8-9, or a subsequence thereof having at least 16 consecutive amino acid residues thereof.

18. (New) A mixture according to claim 8, the <sup>1st</sup> polypeptide comprising at least one sequence selected from the group consisting of SEQ ID NOS:8-9, or a subsequence thereof having at least 64 consecutive amino acid residues thereof.

19. (New) A mixture according to claim 8, the <sup>1st</sup> polypeptide comprising at least one sequence selected from the group consisting of SEQ ID NOS:10-11, or a subsequence thereof having at least 16 consecutive amino acid residues thereof.

20. (New) A mixture according to claim 8, the <sup>1st</sup> polypeptide comprising at least one sequence selected from the group consisting of SEQ ID NOS:10-11, or a subsequence thereof having at least 64 consecutive amino acid residues thereof.

21. (New) A mixture according to claim 8, the <sup>1st</sup> polypeptide comprising at least one sequence selected from the group consisting of SEQ ID NOS:12-14, or a subsequence thereof having at least 16 consecutive amino acid residues thereof.

6.  
22. (New) A mixture according to claim 8, the <sup>1</sup> ~~Slit~~ <sup>first</sup> polypeptide comprising at least one sequence selected from the group consisting of SEQ ID NOS:12-14, or a subsequence thereof having at least 64 consecutive amino acid residues thereof.

16.  
23. (New) A mixture according to claim 8, the <sup>1</sup> ~~Slit~~ <sup>first</sup> polypeptide comprising at least one sequence selected from the group consisting of SEQ ID NO:2, amino acid residues 1-10; SEQ ID NO:2, amino acid residues 29-41; SEQ ID NO:2, amino acid residues 75-87; SEQ ID NO:2, amino acid residues 92-109; SEQ ID NO:2, amino acid residues 132-141; SEQ ID NO:2, amino acid residues 192-205; SEQ ID NO:2, amino acid residues 258-269; SEQ ID NO:2, amino acid residues 295-311; SEQ ID NO:2, amino acid residues 316-330; SEQ ID NO:2, amino acid residues 373-382; SEQ ID NO:2, amino acid residues 403-422; SEQ ID NO:2, amino acid residues 474-485; SEQ ID NO:2, amino acid residues 561-576; SEQ ID NO:2, amino acid residues 683-697; SEQ ID NO:2, amino acid residues 768-777; SEQ ID NO:2, amino acid residues 798-813; SEQ ID NO:2, amino acid residues 882-894; SEQ ID NO:2, amino acid residues 934-946; SEQ ID NO:2, amino acid residues 1054-1067; SEQ ID NO:2, amino acid residues 1181-1192; SEQ ID NO:2, amino acid residues 1273-1299; SEQ ID NO:2, amino acid residues 1383-1397; SEQ ID NO:2, amino acid residues 1468-1477; and SEQ ID NO:2, amino acid residues 1508-1517.

17.  
24. (New) A mixture according to claim 8, comprising a cell comprising the <sup>Second</sup> ~~Robo~~ polypeptide.

25 18.  
24. (New) A mixture according to claim 10, comprising a cell comprising the <sup>3</sup> ~~Robo~~ <sup>Second</sup> polypeptide.

26 19.  
25. (New) A mixture according to claim 8, comprising a candidate agent for modulating an interaction of the Robo and Slit polypeptides.

27 20.  
26. (New) A method of identifying agents which modulate the interaction of a ~~Robo~~ <sup>Second</sup> polypeptide and a Slit polypeptide, said method comprising the steps of:  
combining the mixture of claim 8 and a candidate agent under conditions whereby, but for the presence of the agent, the <sup>Second</sup> ~~Robo~~ and <sup>First</sup> ~~Slit~~ polypeptides engage in a first interaction, and determining a second interaction of the <sup>Second</sup> ~~Robo~~ and <sup>First</sup> ~~Slit~~ polypeptides in the presence of the agent,